

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

- (A) NAME: DANISCO A/S
(B) STREET: Langebrogade 1
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(E) COUNTRY: Denmark
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15 (ii) TITLE OF INVENTION: Cloning and use of Lipase 3 gene from
Aspergillus tubigenis

(iii) NUMBER OF SEQUENCES: 9

20

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Aspergillus tubigenis

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Val Ser Thr Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp
 1 5 10 15
 Ser Ala Ala Ala Tyr Xaa Ser Asn Asn
 20 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus tubigensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Val His Thr Gly Phe Trp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus tubigensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Trp Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys
5 1 5 10

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTCCARAANC CNGTRTGNAC

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25 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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CARYTNTTYG CNCARTGG

18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 5 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCVGCHSWYT CCCAVGC

17

15 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR fragment"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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CAGTTGTTGC CGCAATGGTC TGCCGCAGCT TATTGCTCGA ATAATATCGA CTCGAAAGAV 60

TCCAACTGA CATGCACGGC CAACGCCTGT CCATCAGTCG AGGAGGCCAG TACCACGATG 120

35 CTGCTGGAGT TCGACCTGTA TGCTACTCAG ATCGCAGACA TAGAGCACAG CTAATTGAAC 180

AGGACGAACG ACTTTTGGAG GCACAGCCGG TTTCCTGGCC GCGGACAACA CCAACAAGCG 240

GCTCGTGGTC GCCTTCCGGG GAAGCAGCAC GATTGAGAAC TGGATTGCTA ATCYTGACTT 300

40

CATCCTGGRA GATAACG

317

(2) INFORMATION FOR SEQ ID NO: 8:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus tubigenensis*

10 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(1..82, 135..300, 347..683, 737..1045)

(ix) FEATURE:

15 (A) NAME/KEY: sig_peptide

(B) LOCATION: 1..81

(ix) FEATURE:

20 (A) NAME/KEY: mat_peptide

(B) LOCATION: join(82, 135..300, 347..683, 737..1042)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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25 ATG TTC TCT GGA CGG TTT GGA GTG CTT TTG ACA GCG CTT GCT GCG CTG      48
   Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu
   -27   -25           -20           -15

   GGT GCT GCC GCG CCG GCA CCG CTT GCT GTG CGG A GTAGGTGTGC      92
30 Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg
   -10           -5

   CCGATGTGAG ATGGTTGGAT AGCACTGATG AAGGGTGAAT AG  GT GTC TCG ACT      145
                                   Ser Val Ser Thr
35                                   1

   TCC ACG TTG GAT GAG TTG CAA TTG TTC GCG CAA TGG TCT GCC GCA GCT      193
   Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala
   5           10           15           20

40 TAT TGC TCG AAT AAT ATC GAC TCG AAA GAC TCC AAC TTG ACA TGC ACG      241
   Tyr Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr
           25           30           35

45 GCC AAC GCC TGT CCA TCA GTC GAG GAG GCC AGT ACC ACG ATG CTG CTG      289
   Ala Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu

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	40	45	50	
	GAG TTC GAC CT	GTATGTCAC	T CAGATCGCAG	ACATAGAGCA CAGCTAATTT 340
	Glu Phe Asp Leu			
5	55			
	GAACAG G ACG AAC GAC TTT GGA GGC ACA GCC GGT TTC CTG GCC GCG GAC	389		
	Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala Asp			
	60	65	70	
10				
	AAC ACC AAC AAG CGG CTC GTG GTC GCC TTC CGG GGA AGC AGC ACG ATT	437		
	Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr Ile			
	75	80	85	
15	GAG AAC TGG ATT GCT AAT CTT GAC TTC ATC CTG GAA GAT AAC GAC GAC	485		
	Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp Asp			
	90	95	100	
	CTC TGC ACC GGC TGC AAG GTC CAT ACT GGT TTC TGG AAG GCA TGG GAG	533		
20	Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp Glu			
	105	110	115	
	TCC GCT GCC GAC GAA CTG ACG AGC AAG ATC AAG TCT GCG ATG AGC ACG	581		
	Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser Thr			
25	120	125	130	
	TAT TCG GGC TAT ACC CTA TAC TTC ACC GGG CAC AGT TTG GGC GGC GCA	629		
	Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly Ala			
	135	140	145	150
30	TTG GCT ACG CTG GGA GCG ACA GTT CTG CGA AAT GAC GGA TAT AGC GTT	677		
	Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser Val			
	155	160	165	
35	GAG CTG GTGAGTCCTT CACAAAGGTG ATGGAGCGAC AATCGGGAAC AGACAGTCAA	733		
	Glu Leu			
	TAG TAC ACC TAT GGA TGT CCT CGA ATC GGA AAC TAT GCG CTG GCT GAG	781		
40	Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu Ala Glu			
	170	175	180	
	CAT ATC ACC AGT CAG GGA TCT GGG GCC AAC TTC CGT GTT ACA CAC TTG	829		
	His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr His Leu			
45	185	190	195	

AAC GAC ATC GTC CCC CGG GTG CCA CCC ATG GAC TTT GGA TTC AGT CAG 877
 Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe Ser Gln
 5 200 205 210 215

 CCA AGT CCG GAA TAC TGG ATC ACC AGT GGC AAT GGA GCC AGT GTC ACG 925
 Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser Val Thr
 220 225 230
 10
 GCG TCG GAT ATC GAA GTC ATC GAG GGA ATC AAT TCA ACG GCG GGA AAT 973
 Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala Gly Asn
 235 240 245
 15 GCA GGC GAA GCA ACG GTG AGC GTT GTG GCT CAC TTG TGG TAC TTT TTT 1021
 Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr Phe Phe
 250 255 260

 GCG ATT TCC GAG TGC CTG CTA TAA 1045
 20 Ala Ile Ser Glu Cys Leu Leu *
 265 270

(2) INFORMATION FOR SEQ ID NO: 9:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu
 35 -27 -25 -20 -15

 Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg Ser Val Ser Thr Ser
 -10 -5 1 5
 40 Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala Tyr
 10 15 20

 Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr Ala
 25 30 35
 45
 Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu Glu

	40		45		50
	Phe Asp Leu Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala				
	55		60		65
5	Asp Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr				
	70	75	80		85
	Ile Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp				
10		90	95		100
	Asp Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp				
		105	110		115
15	Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser				
		120	125		130
	Thr Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly				
		135	140		145
20	Ala Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser				
		150	155	160	165
	Val Glu Leu Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu				
25		170	175		180
	Ala Glu His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr				
		185	190		195
30	His Leu Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe				
		200	205		210
	Ser Gln Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser				
		215	220		225
35	Val Thr Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala				
		230	235	240	245
	Gly Asn Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr				
40		250	255		260
	Phe Phe Ala Ile Ser Glu Cys Leu Leu *				
		265	270		